ORIGINAL PAPERS

Genome analysis
The null hypothesis of GSEA, and a novel statistical model for competitive gene set analysis
B.Debrabant

A general framework for association analysis of microbial communities on a taxonomic tree
Z.-Z.Tang, G.Chen, A.V.Alekseyenko and H.Li

An informative approach on differential abundance analysis for time-course metagenomic sequencing data
D.Luo, S.Ziebell and L.An

A new method for decontamination of de novo transcriptomes using a hierarchical clustering algorithm

VarMatch: robust matching of small variant datasets using flexible scoring schemes
C.Sun and P.Medvedev

Sequence analysis
A new method for decontamination of de novo transcriptomes using a hierarchical clustering algorithm

VarMatch: robust matching of small variant datasets using flexible scoring schemes
C.Sun and P.Medvedev

Development and application of an algorithm to compute weighted multiple glycan alignments
M.Hascio, Y.Kikuta and K.F.Ashk-Kinosita

ntCard: a streaming algorithm for cardinality estimation in genomics data
H.Movahdat, H.Khan and I.Broll

Protein multiple sequence alignment benchmarking through secondary structure prediction
Q.Le, T.Sievers and D.O.Higgins

Systems biology
Linearity of network proximity measures: implications for set-based queries and significance testing
S.Maxwell, M.K.Chance and M.Koyuturk

Modeling gene-wise dependencies improves the identification of drug response biomarkers in cancer studies
O.Nikolova, R.Moser, C.Kemp, M.Gönen and A.A.Margolin

PhenoCurve: capturing dynamic phenotype-environment relationships using phenomics data
Y.Yang, L.Xu, Z.Feng, J.A.Cruz, L.Savage, D.M.Kramer and J.Chen

Image-based correction of continuous and discontinuous non-planar axial distortion in serial section microscopy
P.Hanslovsky, J.A.Bogovic and S.Saalfeld

APPLICATIONS NOTES

Genome analysis
The genetic map comparator: a user-friendly application to display and compare genetic maps
Y.Holtz, J.L.David and V.Ranwez

VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis

CircosVCF: circos visualization of whole-genome sequence variations stored in VCF files
E.Drori, D.Levy, P.Smirin-Yosef, O.Rahimi and M.Salmon Divon

Edlib: a C/C++ library for fast, exact sequence alignment using edit distance
M.Sodicc and M.Swik

AFS: identification and quantification of species composition by metagenomic sequencing

fastMitoCalc: an ultra-fast program to estimate mitochondrial DNA copy number from whole-genome sequences
Y.Qian, T.J.Butler, K.Opsahl-Ong, N.S.Giroux, C.Sidore, R.Nagaraja, F.Cucca, L.Ferrucci, G.R.Abecasis, D.Schlessinger and J.Ding

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